



<110> Cervin, Marguerite A.
Soucaille, Philippe
Valle, Fernando
Whited, Gregory M.

<120> Glucose Transport Mutants for Production
of Biomaterial

<130> GC778-2

<140> US 10/728,337

<141> 2003-12-03

<150> US 60/416,166

<151> 2002-10-04

<150> US 60/374,931

<151> 2002-10-04

<160> 27

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> GalP-ptrc DNA cassette

<400> 1

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taaaaaataa	ccatattgga	gggcatcatg				1350

<210> 2

<211> 364

<212> DNA

<213> Artificial Sequence

<220>

<223> galP-trc DNA cassette after removal of CAT gene

<400> 2

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<210> 3

<211> 1352

<212> DNA

<213> Artificial Sequence

<220>

<223> glk-trc DNA cassette

<400> 3

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<210> 4

<211> 13669

<212> DNA

<213> Artificial Sequence

<220>

<223> pSYCO101 plasmid

<400> 4

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Ser Asn Lys Ala Met Thr Phe Phe Val Cys Phe Leu Ala Ala Leu Ala
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Phe Ile Ala Asp Glu Phe Gln Ile Thr Ser His Thr Gln Glu Trp Val
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Val Ser Ser Met Met Phe Gly Ala Ala Val Gly Ala Val Gly Ser Gly
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Trp Leu Ser Phe Lys Leu Gly Arg Lys Lys Ser Leu Met Ile Gly Ala
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Ile Leu Phe Val Ala Gly Ser Leu Phe Ser Ala Ala Ala Pro Asn Val
90                      95                      100                      105
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Ala Ser Tyr Thr Ala Pro Leu Tyr Leu Ser Glu Ile Ala Pro Glu Lys
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Ile Arg Gly Ser Met Ile Ser Met Tyr Gln Leu Met Ile Thr Ile Gly
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Leu Val Asn Leu Tyr Arg Ala Ile Val Lys Ala Asp Asn Arg Leu Pro	
660 665 670	
gaa aat ctc aag cca aaa gat att acc gaa cgc gcg ctg gct gac agc	2658
Glu Asn Leu Lys Pro Lys Asp Ile Thr Glu Arg Ala Leu Ala Asp Ser	
675 680 685 690	
tgc acc gat tgc cgc cgc gca ttg tcg ctg ttt tgc gtc att atg ggc	2706
Cys Thr Asp Cys Arg Arg Ala Leu Ser Leu Phe Cys Val Ile Met Gly	
695 700 705	
cgt ttt ggc ggc aat ctg gcg ctc aat ctc ggg aca ttt ggc ggc gtg	2754
Arg Phe Gly Gly Asn Leu Ala Leu Asn Leu Gly Thr Phe Gly Gly Val	
710 715 720	
ttt att gcg ggc ggt atg ctg ccg cgc ttc ctt gag ttc ttc aaa ggc	2802
Phe Ile Ala Gly Gly Met Leu Pro Arg Phe Leu Glu Phe Phe Lys Gly	
725 730 735	
tcc ggt ttc cgt gcc gca ttt gaa gat aaa ggc cgc ttt aaa gaa tat	2850
Ser Gly Phe Arg Ala Ala Phe Glu Asp Lys Gly Arg Phe Lys Glu Tyr	
740 745 750	
gtc cat gat att ccg gtg tat ctc atc gtc cat gac aat ccg ggc ctt	2898
Val His Asp Ile Pro Val Tyr Leu Ile Val His Asp Asn Pro Gly Leu	
755 760 765 770	
ctc ggt tcc ggt gca cat tta cgc cag acc tta ggt cac att ctg	2943
Leu Gly Ser Gly Ala His Leu Arg Gln Thr Leu Gly His Ile Leu	
775 780 785	
taaataccttc cttttatatc gggaggtaac tctcccgata atctttttaa tcatacagtt	3003

tattcaattt ttctttgtgt cccctcaciaa ggctcgac

3040

<210> 26
 <211> 464
 <212> PRT
 <213> Unknown

<220>
 <223> galP amino acid sequence

<400> 26
 Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn Lys Ala Met Thr Phe
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 Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp
 20 25 30
 Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln
 35 40 45
 Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly
 50 55 60
 Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly
 65 70 75 80
 Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser
 85 90 95
 Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg
 100 105 110
 Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu
 115 120 125
 Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
 130 135 140
 Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser
 145 150 155 160
 Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val
 165 170 175
 Ile Ile Ile Pro Ala Ile Leu Leu Leu Ile Gly Val Phe Phe Leu Pro
 180 185 190
 Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu
 195 200 205
 Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu
 210 215 220
 Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala
 225 230 235 240
 Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val
 245 250 255
 Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr
 260 265 270
 Tyr Ala Pro Lys Ile Phe Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu
 275 280 285
 Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr
 290 295 300
 Phe Ile Ala Ile Gly Leu Val Asp Arg Trp Gly Arg Lys Pro Thr Leu
 305 310 315 320
 Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr
 325 330 335
 Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile
 340 345 350
 Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro
 355 360 365

Leu	Ile	Trp	Val	Leu	Cys	Ser	Glu	Ile	Gln	Pro	Leu	Lys	Gly	Arg	Asp
370						375					380				
Phe	Gly	Ile	Thr	Cys	Ser	Thr	Ala	Thr	Asn	Trp	Ile	Ala	Asn	Met	Ile
385					390					395					400
Val	Gly	Ala	Thr	Phe	Leu	Thr	Met	Leu	Asn	Thr	Leu	Gly	Asn	Ala	Asn
				405					410					415	
Thr	Phe	Trp	Val	Tyr	Ala	Ala	Leu	Asn	Val	Leu	Phe	Ile	Leu	Leu	Thr
			420					425					430		
Leu	Trp	Leu	Val	Pro	Glu	Thr	Lys	His	Val	Ser	Leu	Glu	His	Ile	Glu
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<210> 27
 <211> 321
 <212> PRT
 <213> Unknown

<220>
 <223> Glk amino acid sequence

<400> 27

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Tyr	Ser	Gly	Leu	Asp	Tyr	Pro	Ser	Leu	Glu	Ala	Val	Ile	Arg	Val	Tyr
		35					40					45			
Leu	Glu	Glu	His	Lys	Val	Glu	Val	Lys	Asp	Gly	Cys	Ile	Ala	Ile	Ala
	50					55				60					
Cys	Pro	Ile	Thr	Gly	Asp	Trp	Val	Ala	Met	Thr	Asn	His	Thr	Trp	Ala
65					70					75					80
Phe	Ser	Ile	Ala	Glu	Met	Lys	Lys	Asn	Leu	Gly	Phe	Ser	His	Leu	Glu
				85					90					95	
Ile	Ile	Asn	Asp	Phe	Thr	Ala	Val	Ser	Met	Ala	Asn	Pro	Met	Leu	Lys
			100					105					110		
Lys	Glu	His	Leu	Ile	Gln	Phe	Gly	Gly	Ala	Glu	Pro	Val	Glu	Gly	Lys
		115					120					125			
Pro	Ile	Ala	Val	Tyr	Gly	Ala	Gly	Thr	Gly	Leu	Gly	Val	Ala	His	Leu
	130				135					140					
Val	His	Val	Asp	Lys	Arg	Trp	Val	Ser	Leu	Pro	Gly	Glu	Gly	Gly	His
145				150					155						160
Val	Asp	Phe	Ala	Pro	Asn	Ser	Glu	Glu	Glu	Ala	Ile	Ile	Leu	Glu	Ile
				165					170					175	
Leu	Arg	Ala	Glu	Ile	Gly	His	Val	Ser	Ala	Glu	Ala	Cys	Leu	Ser	Gly
		180						185					190		
Pro	Gly	Leu	Val	Asn	Leu	Tyr	Arg	Ala	Ile	Val	Lys	Ala	Asp	Asn	Arg
		195					200					205			
Leu	Pro	Glu	Asn	Leu	Lys	Pro	Lys	Asp	Ile	Thr	Glu	Arg	Ala	Leu	Ala
	210					215					220				
Asp	Ser	Cys	Thr	Asp	Cys	Arg	Arg	Ala	Leu	Ser	Leu	Phe	Cys	Val	Ile
225					230					235					240
Met	Gly	Arg	Phe	Gly	Gly	Asn	Leu	Ala	Leu	Asn	Leu	Gly	Thr	Phe	Gly
				245					250					255	
Gly	Val	Phe	Ile	Ala	Gly	Gly	Ile	Val	Pro	Arg	Phe	Leu	Glu	Phe	Phe
			260					265					270		
Lys	Gly	Ser	Gly	Phe	Arg	Ala	Ala	Phe	Glu	Asp	Lys	Gly	Arg	Phe	Lys

		275					280					285					
Glu	Tyr	Val	His	Asp	Ile	Pro	Val	Tyr	Leu	Ile	Val	His	Asp	Asn	Pro		
	290					295					300						
Gly	Leu	Leu	Gly	Ser	Gly	Ala	His	Leu	Arg	Gln	Thr	Leu	Gly	His	Ile		
305					310					315					320		
Leu																	